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SEQUENCE LISTING

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Wong, Chi-Wai
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<120> Methods of Diagnosing & Treating Diabetes and Insulin Resistance

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<140> US 10/516,803
<141> 2004-12-02

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<151> 2002-06-04

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 (PTPLA)

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precursor, cysteine-rich motorneuron 1 (CRIM1)
cDNA

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<213> Mus musculus
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cysteine-rich motorneuron 1 (CRIM1), partial

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35 40 45

Gly Val Cys Gly Cys Cys Tyr Met Cys Ala Arg Gln Arg Asn Glu Ser
50 55 60

Cys Gly Gly Ala Tyr Gly Leu His Gly Ala Cys Asp Arg Gly Leu Arg
 65 70 75 80

Cys Val Ile Arg Pro Pro Leu Asn Gly Asp Ser Ile Thr Glu Tyr Glu
 85 90 95

Val Gly Val Cys Glu Asp Glu Asp Trp Asp Asp Asp Gln Leu Ile Gly
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Phe Glu Pro Cys Asn Glu Asn Leu Ile Ser Gly Cys Asn Ile Ile Asn
 115 120 125

Gly Lys Cys Glu Cys Gly Thr Ile Arg Thr Cys Asn Asn Pro Phe Glu
130 135 140

Phe	Pro	Arg	Lys	Asp	Met	Cys	Leu	Ser	Ala	Leu	Lys	Arg	Ile	Glu	Glu
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Arg Cys Pro Glu Asp Ser Ile Leu Ile Glu Gly Tyr Ala Pro Pro Gly
 180 185 190
 Glu Cys Cys Pro Leu Pro Ser Arg Cys Val Cys Asp Pro Ala Gly Cys
 195 200 205
 Leu Arg Lys Val Cys Gln Pro Gly Tyr Leu Asn Ile Leu Val Ser Lys
 210 215 220
 Ala Ser Gly Lys Pro Gly Glu Cys Cys Asp Leu Tyr Glu Cys Lys Pro
 225 230 235 240
 Val Phe Ser Val Asp Cys Ser Thr Val Glu Cys Pro Pro Val Gln Gln
 245 250 255
 Ala Val Cys Pro Leu Asp Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala
 260 265 270
 Asp Gly Cys Cys Thr Leu Pro Ala Arg Cys Glu Cys Leu Ser Gly Leu
 275 280 285
 Cys Gly Phe Pro Val Cys Glu Val Gly Ser Thr Pro Arg Ile Val Ser
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 Arg Gly Asp Gly Thr Pro Gly Lys Cys Cys Asp Val Phe Glu Cys Val
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 Asn Glu Thr Lys Pro Ala Cys Val Phe Asn Ser Val Glu Tyr Tyr Asp
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 Gly Asp Met Phe Arg Met Asp Asn Cys Arg Phe Cys Arg Cys Gln Gly
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 Gly Val Ser Ile Cys Phe Thr Ala Gln Cys Gly Glu Leu Asn Cys Glu
 355 360 365
 Arg Tyr Tyr Val Pro Glu Gly Glu Cys Cys Pro Val Cys Glu Asp Pro
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 Ile Tyr Pro Leu Asn Asn Pro Ala Gly Cys Tyr Ala Asn Gly Gln Ile
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 Arg Ala His Gly Asp Arg Trp Arg Glu Asp Asp Cys Thr Phe Cys Gln
 405 410 415
 Cys Ile Asn Gly Glu Pro His Cys Val Ala Thr Ala Cys Gly Gln Ser
 420 425 430
 Cys Met His Pro Val Lys Val Pro Gly Glu Cys Cys Pro Val Cys Glu
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 Glu Pro Thr Tyr Ile Thr Ile Asp Pro Pro Ala Cys Gly Glu Leu Ser
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Thr Asp Val His Asn Cys Glu Leu Cys Gln Cys Arg Pro Arg Pro Lys
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Gly Cys Leu Ile Cys Lys Cys Arg Glu Val Pro Pro Ser Ala Gly Pro
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Pro Val Leu Ser Gly Thr Cys Leu Ser Met Asp Gly His His His Lys
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Gly Lys Glu Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly
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Asn Pro Thr Ile Arg Ser Gly Gln Cys Cys Pro Ser Cys Thr Asp Asp
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Phe Val Val Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala
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Pro Gly Gly Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser
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Cys Thr Gln Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu
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Val Cys Pro Pro Leu Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser
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Cys Cys Pro Gln Cys Thr Asp Asp Pro Pro Gln Pro Ser Thr Ser His
 725 730 735

Asn Glu Ser Val Pro Ser Tyr Cys Arg Asn Asp Glu Gly Asp Ile Phe
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Leu Ala Ala Glu Ser Trp Lys Pro Asp Ala Cys Thr Ser Cys Val Cys
 755 760 765

Val Asp Ser Ala Ile Ser Cys Tyr Ser Glu Ser Cys Pro Ser Val Ala
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Cys Glu Arg Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Leu
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Glu Asp Thr Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Thr
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 Pro Cys Ala Glu Pro Ile Lys Val Glu Gly Ser Cys Cys Pro Met Cys
 850 855 860
 Pro Glu Met Tyr Val Pro Glu Pro Thr Asn Val Pro Ile Glu Lys Lys
 865 870 875 880
 Asn His Arg Gly Glu Ile Asp Leu Glu Val Pro Met Trp Pro Thr Pro
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 Val Asp Tyr Arg Asp Asn Asn Arg Leu His Pro Gly Glu Asp Ser Ser
 915 920 925
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 965 970 975
 Gln Leu Val Ser Val Asp Cys Lys Lys Gly Thr Arg Val Gln Val Asp
 980 985 990
 Gly Pro Gln Arg Met Leu Arg Ile Ala Glu Pro Asp Ala Arg Phe Ser
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 (PPP3CA) cDNA

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 phosphatase catalytic subunit, calcineurin A alpha
 (PPP3CA)

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Glu Val Phe Asp Asn Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala
 35 40 45

His Leu Met Lys Glu Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile
 50 55 60

Ile Thr Glu Gly Ala Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp
 65 70 75 80
 Ile Asp Ala Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe
 85 90 95
 Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
 100 105 110
 Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
 115 120 125
 Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
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 Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
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 Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp
 165 170 175
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 180 185 190
 Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
 195 200 205
 Leu Asp Asp Ile Arg Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr
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 Gly Pro Met Cys Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly
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 245 250 255
 Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Glu Phe Leu Gln His Asn
 260 265 270
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 Ser Pro His Pro Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp
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 405 410 415
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 Pro Ser Gly Val Leu Ser Gly Gly Lys Gln Thr Leu Gln Ser Ala Thr
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 His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn
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 Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn Leu
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      (PPP3CA) cDNA

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<223> CTGF

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 <213> Mus musculus

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 phosphatase catalytic subunit, calcineurin A alpha
 (PPP3CA)

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Val	Val	Lys	Ala	Val	Pro	Phe	Pro	Pro	Ser	His	Arg	Leu	Thr	Ala	Lys
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Glu	Val	Phe	Asp	Asn	Asp	Gly	Lys	Pro	Arg	Val	Asp	Ile	Leu	Lys	Ala
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															40
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His	Leu	Met	Lys	Glu	Gly	Arg	Leu	Glu	Ser	Val	Ala	Leu	Arg	Ile

															50
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Ile	Thr	Glu	Gly	Ala	Ser	Ile	Leu	Arg	Gln	Glu	Lys	Asn	Leu	Leu	Asp
															65

															70
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															75
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Ile	Asp	Ala	Pro	Val	Thr	Val	Cys	Gly	Asp	Ile	His	Gly	Gln	Phe	Phe
															85

															90
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															95
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Asp	Leu	Met	Lys	Leu	Phe	Glu	Val	Gly	Gly	Ser	Pro	Ala	Asn	Thr	Arg
															100

															105
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															110
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Tyr	Leu	Phe	Leu	Gly	Asp	Tyr	Val	Asp	Arg	Gly	Tyr	Phe	Ser	Ile	Glu
															115

															120
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															125
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Cys	Val	Leu	Tyr	Leu	Trp	Ala	Leu	Lys	Ile	Leu	Tyr	Pro	Lys	Thr	Leu
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															135
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															140
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 Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
 195 200 205
 Leu Asp Asp Ile Arg Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr
 210 215 220
 Gly Pro Met Cys Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly
 225 230 235 240
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 245 250 255
 Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Asp Phe Leu Gln His Asn
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His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn
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Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn Leu
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<212> DNA

<213> Rattus norvegicus

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phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA) cDNA

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<222> (271)..(1806)

<223> PPP3CA

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phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA)

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Ile Asp Ala Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe
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Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
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Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
115 120 125

Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
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Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
145 150 155 160

Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp
165 170 175

Ala Cys Met Asp Ala Phe Asp Cys Leu Pro Leu Ala Ala Leu Met Asn
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Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
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<213> Homo sapiens

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      type 3 (PTPN3a) cDNA

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<222> (24)..(2765)
<223> PTPN3a

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<212> PRT
<213> *Homo sapiens*

<220>
<223> human protein tyrosine phosphatase, non-receptor
type 3 (PTPN3a)

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Asp Thr Gly Gln Val Leu Leu Asp Met Val His Asn His Leu Gly Val
      50          55          60

Thr Glu Lys Glu Tyr Phe Gly Leu Gln His Asp Asp Asp Ser Val Asp
      65          70          75          80

Ser Pro Arg Trp Leu Glu Ala Ser Lys Pro Ile Arg Lys Gln Leu Lys
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Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Phe Phe Ile Pro
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Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe Leu
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Gln Leu Lys Met Asp Ile Cys Glu Gly Arg Leu Thr Cys Pro Leu Asn
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 180 185 190
 Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr Ile
 195 200 205
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 Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala Gly
 225 230 235 240
 Val Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp Val
 245 250 255
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Pro Gly Ser Cys Ser Pro Asp Gly Val Asp Gln Gln Leu Leu Asp Asp
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Phe His Arg Val Thr Lys Gly Gly Ser Thr Glu Asp Ala Ser Gln Tyr
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Tyr Cys Asp Lys Asn Asp Asn Gly Asp Ser Tyr Leu Val Leu Ile Arg
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Ile Thr Pro Asp Glu Asp Gly Lys Phe Gly Phe Asn Leu Lys Gly Gly
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Val Asp Gln Lys Met Pro Leu Val Val Ser Arg Ile Asn Pro Glu Ser
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Pro Ala Asp Thr Cys Ile Pro Lys Leu Asn Glu Gly Asp Gln Ile Val
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Leu Ile Asn Gly Arg Asp Ile Ser Glu His Thr His Asp Gln Val Val
 565 570 575

Met Phe Ile Lys Ala Ser Arg Glu Ser His Ser Arg Glu Leu Ala Leu
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Val Ile Arg Arg Ala Val Arg Ser Phe Ala Asp Phe Lys Ser Glu
 595 600 605

Asp Glu Leu Asn Gln Leu Phe Pro Glu Ala Ile Phe Pro Met Cys Pro
 610 615 620

Glu Gly Gly Asp Thr Leu Glu Gly Ser Met Ala Gln Leu Lys Lys Gly
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Lys Pro Gly Leu Ala Ile Thr Phe Ala Lys Leu Pro Gln Asn Leu Asp
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Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr Asp Thr Thr Arg Val Leu
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Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val Asn Met Glu
 690 695 700

Ile Pro Ala Ala Asn Leu Val Asn Lys Tyr Ile Ala Thr Gln Gly Pro
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Lys Cys His Gln Tyr Trp Pro Asp Pro Pro Asp Val Met Asn His Gly
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Gly Phe His Ile Gln Cys Gln Ser Glu Asp Cys Thr Ile Ala Tyr Val
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Ser Arg Glu Met Leu Val Thr Asn Thr Gln Thr Gly Glu Glu His Thr
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Val Thr His Leu Gln Tyr Val Ala Trp Pro Asp His Gly Ile Pro Asp
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Asp Ser Ser Asp Phe Leu Glu Phe Val Asn Tyr Val Arg Ser Leu Arg
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Val Asp Ser Glu Pro Val Leu Val His Cys Ser Ala Gly Ile Gly Arg
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Thr Gly Val Leu Val Thr Met Glu Thr Ala Met Cys Leu Thr Glu Arg
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Asn Leu Pro Ile Tyr Pro Leu Asp Ile Val Arg Lys Met Arg Asp Gln
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 <213> Mus musculus

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 type 3 (PTPN3) cDNA

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 <222> (1)..(3087)
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<213> Mus musculus

<220>

<223> mouse protein tyrosine phosphatase, non-receptor type 3 (PTPN3)

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 20 25 30

Arg Thr Val Gly Trp Glu Tyr Glu Val Lys Gln Leu Phe Ser Gly Lys
 35 40 45

Leu Ala Arg Lys Tyr Ile Pro Asp Ser Ser Asp Ile Phe Ile Glu Lys
50 55 60

Gly Met Val Glu Val Val Gly Tyr Ser Ala Ala Val Met Thr Ser Arg
 65 70 75 80

Leu Arg Ala Leu Gly Gly Arg Ile Asn Asn Thr Arg Thr Ser Glu Leu
 85 90 95

 Pro Lys Glu Lys Thr Arg Ser Glu Val Ile Cys Ser Ile Arg Phe Leu
 100 105 110

 Asp Gly Leu Val Gln Thr Phe Lys Val Asn Lys Gln Asp Leu Gly Gln
 115 120 125

 Ser Leu Leu Asp Met Ala Tyr Gly His Leu Gly Val Thr Glu Lys Glu
 130 135 140

 Tyr Phe Gly Leu Gln His Gly Asp Asp Pro Val Asp Ser Pro Arg Trp
 145 150 155 160

 Leu Glu Ala Ser Lys Pro Leu Arg Lys Gln Leu Lys Gly Glu Tyr Ala
 165 170 175

 Leu Ala Ser Leu Gly Arg Trp Val Tyr Gly Lys Leu Ser Ser Pro Tyr
 180 185 190

 Gly Gly Leu Lys Val Ala Gly Lys Pro Asn Leu Phe Leu Lys Asn Val
 195 200 205

 Val Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Tyr Phe Ile
 210 215 220

 Pro Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe.
 225 230 235 240

 Leu Gln Leu Lys Met Asp Val Cys Glu Gly Arg Leu Thr Cys Pro Leu
 245 250 255

 Asn Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly
 260 265 270

 Asp Phe Asn Ser Ser Ile His His Pro Gly Tyr Leu Ala Asp Ser Gln
 275 280 285

 Phe Ile Pro Asp Gln Asn Asp Asp Phe Leu Ser Lys Val Glu Ser Leu
 290 295 300

 His Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr
 305 310 315 320

 Ile Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Gly
 325 330 335

 Gly Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala
 340 345 350

 Gly Ile Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp
 355 360 365

 Lys Lys Phe Phe Ile His Gln Arg Gln Lys Glu Glu Lys Ile Val
 370 375 380

 Ala Val Arg Ser Ser Asp Pro Val Ala Ile Ser Ala Glu Ser Arg Glu
 385 390 395 400

His Ile Val Ala Phe Asn Met Leu Asn Tyr Arg Ser Cys Lys Asn Leu
 405 410 415

 Trp Lys Ser Cys Val Glu His His Ser Phe Phe Gln Ala Lys Lys Leu
 420 425 430

 Leu Pro Gln Glu Lys Asn Val Leu Ser Gln Tyr Trp Thr Leu Gly Ser
 435 440 445

 Arg Asn Pro Lys Lys Ser Val Asn Asn Gln Tyr Cys Lys Lys Val Ile
 450 455 460

 Gly Gly Met Val Trp Asn Pro Val Met Arg Arg Ser Leu Ser Val Glu
 465 470 475 480

 Arg Leu Glu Thr Lys Ser Leu Pro Ser Arg Ser Pro Pro Ile Thr Pro
 485 490 495

 Asn Trp Arg Ser Pro Arg Leu Arg His Glu Ile Arg Lys Pro Arg His
 500 505 510

 Ser Ser Ala Asp Asn Leu Ala Asn Glu Met Thr Tyr Ile Thr Glu Thr
 515 520 525

 Glu Asp Val Phe Tyr Thr Tyr Lys Gly Pro Leu Ser Pro Lys Asp Ser
 530 535 540

 Asp Ser Glu Val Ser Gln Asn His Ser Pro His Arg Glu Ser Leu Ser
 545 550 555 560

 Glu Asn Asn Pro Ala Gln Ser Cys Leu Thr Gln Lys Ser Ser Ser Ser
 565 570 575

 Val Ser Pro Ser Ser Asn Ala Pro Gly Ser Cys Ser Pro Asp Gly Val
 580 585 590

 Asp Gln Arg Phe Leu Glu Asp Tyr His Lys Val Thr Lys Gly Gly Phe
 595 600 605

 Val Glu Asp Ala Ser Gln Tyr Tyr Cys Asp Lys Ser Asp Asp Gly Asp
 610 615 620

 Gly Tyr Leu Val Leu Ile Arg Ile Thr Pro Asp Glu Glu Gly Arg Phe
 625 630 635 640

 Gly Phe Asn Leu Lys Ala Asp Thr Cys Met Pro Lys Leu Asn Glu Gly
 645 650 655

 Asp Gln Ile Val Leu Ile Asn Gly Arg Asp Ile Ser Glu His Thr His
 660 665 670

 Asp Gln Val Val Met Phe Ile Lys Ala Ser Arg Glu Ser His Ser Arg
 675 680 685

 Glu Leu Ala Leu Val Ile Arg Arg Lys Gly Lys Ala Thr Phe Val Gly
 690 695 700

 His Glu Gly Leu Val Pro Ala Arg Ala Val Arg Ser Leu Ala Glu Ile
 705 710 715 720

Arg Ser Glu Asp Glu Leu Ser Gln Leu Phe Pro Glu Ala Met Phe Pro
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 Ala Cys Pro Glu Gly Gly Asp Ser Leu Glu Gly Ser Met Glu Leu Leu
 740 745 750
 Lys Lys Gly Leu Glu Ser Gly Thr Val Leu Ile Gln Phe Glu Gln Leu
 755 760 765
 Tyr Arg Lys Lys Pro Gly Leu Ala Val Ser Phe Ala Lys Leu Pro Gln
 770 775 780
 Asn Leu Asp Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr Asp Thr Thr
 785 790 795 800
 Arg Val Leu Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val
 805 810 815
 Asn Met Glu Met Pro Ala Ala Asn Leu Val Asn Lys Tyr Ile Ala Thr
 820 825 830
 Gln Gly Pro Leu Pro Asn Thr Cys Ala Gln Phe Trp Gln Val Val Trp
 835 840 845
 Asp Gln Lys Leu Ser Leu Val Val Met Leu Thr Thr Leu Thr Glu Arg
 850 855 860
 Gly Arg Thr Lys Cys His Gln Tyr Trp Pro Asp Pro Pro Asp Ile Met
 865 870 875 880
 Asp His Gly Ile Phe His Ile Gln Cys Gln Thr Glu Asp Cys Thr Ile
 885 890 895
 Ala Tyr Val Ser Arg Glu Met Leu Val Thr Asn Thr Glu Thr Gly Glu
 900 905 910
 Glu His Thr Val Thr His Leu Gln Tyr Val Ala Trp Pro Asp His Gly
 915 920 925
 Val Pro Asp Asp Ser Ser Asp Phe Leu Glu Phe Val Lys Tyr Val Arg
 930 935 940
 Ser Leu Arg Val Asp Gly Glu Pro Ala Leu Val His Cys Ser Ala Gly
 945 950 955 960
 Ile Gly Arg Thr Gly Val Leu Val Thr Met Glu Thr Ala Met Cys Leu
 965 970 975
 Ile Glu Arg Asn Leu Pro Val Tyr Pro Leu Asp Ile Val Arg Lys Met
 980 985 990
 Arg Asp Gln Arg Ala Met Met Val Gln Thr Ser Ser Gln Tyr Lys Phe
 995 1000 1005
 Val Cys Glu Ala Ile Leu Arg Val Tyr Glu Glu Gly Leu Val Gln Arg
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 Leu Asp Pro Ser
 1025

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<210> 25
<211> 2607
<212> DNA
<213> Homo sapiens

<220>
<223> human protein tyrosine phosphatase, non-receptor
      type 3 (PTPN3b) splice variant cDNA

<220>
<221> CDS
<222> (1)..(2607)
<223> PTPN3b splice variant

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cagaccttta aagttaactaa acaagacact ggcagggttc ttctggatat ggtgcacaac 180
cacctgggtg tgactgaaaa ggaatatttt ggttacagc atgatgacga ctccgtggac 240
tctccttagat ggctggaaagc aagcaaaacc aatcaggaagc agttaaaaagg aggtttcccc 300
tgtaccctgc attttcgagt aagatttttt atacctgatc ccaacacact gcagcaagaa 360
caaaccaggc acttgttattt cttacaactg aagatggata tttgcgaagg aaggttaacc 420
tgccctctta actcagcagt ggttctagcg tccttatgccc tacaatctca ttttggagac 480
tataattctt ccatacatca tccaggctat ctttccgata gtcactttat acccgatcaa 540
aatgaggact ttttaacaaa agtcgaatct ctgcatgagc agcacagtgg gctaaaacaa 600
tcagaagcag aatccgtcta tatcaacata gcgcggacc ctcacttcta tggagtagaa 660
ctgcacagtg gtagggatct gcacaattt gacctaatttga ttggaattgc ttccgcgggt 720
gttgctgtgt accgaaaata catttgacca agtttctatc cttgggtgaa cattctcaaa 780
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gcggcacact gcattcctaa gctgaaccaa ggggatcaa tcgtgttaat caatggccgg 1560
gacatctcag aacacacgc tgaccaagt gtgtatgtca tcaaagccag cccggagttcc 1620
cactcacggg agctggccct ggtgatcagg aggagagctg tccgctcatt tgctgacttc 1680
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cggttattat tgcagggaaa tgaagattat attaatgcaaa gttacgtgaa catggaaatt 1980
cctgctgctt accttgcgaa caagtacatc gccactcagg ggcctgc gcatacctgt 2040
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tacgtcgat ggcctgacca cggataccca gatgactcct ccgactttct ggaatttggta 2340
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ataggtcgaa ccggtgtgtt ggtcactatg gaaacagcca tggcctaaac tggagggaaac 2460
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tttagtccaaa tgctggatcc tagttaa                                         2607

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<210> 26
 <211> 868
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human protein tyrosine phosphatase, non-receptor
 type 3 (PTPN3b) splice variant

<400> 26
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Thr Ser Glu Leu Pro Lys Glu Lys Thr Arg Ser Glu Val Ile Cys Ser
 20 25 30

Ile His Phe Leu Asp Gly Val Val Gln Thr Phe Lys Val Thr Lys Gln
 35 40 45

Asp Thr Gly Gln Val Leu Leu Asp Met Val His Asn His Leu Gly Val
 50 55 60

Thr Glu Lys Glu Tyr Phe Gly Leu Gln His Asp Asp Asp Ser Val Asp
 65 70 75 80

Ser Pro Arg Trp Leu Glu Ala Ser Lys Pro Ile Arg Lys Gln Leu Lys
 85 90 95

Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Phe Phe Ile Pro
 100 105 110

Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe Leu
 115 120 125

Gln Leu Lys Met Asp Ile Cys Glu Gly Arg Leu Thr Cys Pro Leu Asn
 130 135 140

Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly Asp
 145 150 155 160

Tyr Asn Ser Ser Ile His His Pro Gly Tyr Leu Ser Asp Ser His Phe
 165 170 175

Ile Pro Asp Gln Asn Glu Asp Phe Leu Thr Lys Val Glu Ser Leu His
 180 185 190

Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr Ile
 195 200 205

Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Ser Gly
 210 215 220

Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala Gly
 225 230 235 240

Val Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp Val
 245 250 255

Asn Ile Leu Lys Ile Ser Phe Lys Arg Lys Lys Phe Phe Ile His Gln
 260 265 270

Arg Gln Lys Gln Ala Glu Ser Arg Glu His Ile Val Ala Phe Asn Met
 275 280 285
 Leu Asn Tyr Arg Ser Cys Lys Asn Leu Trp Lys Ser Cys Val Glu His
 290 295 300
 His Thr Phe Phe Gln Ala Lys Lys Leu Leu Pro Gln Glu Lys Asn Val
 305 310 315 320
 Leu Ser Gln Tyr Trp Thr Met Gly Ser Arg Asn Thr Lys Lys Arg Ser
 325 330 335
 Pro Arg Leu Arg His Glu Ile Arg Lys Pro Arg His Ser Ser Ala Asp
 340 345 350
 Asn Leu Ala Asn Glu Met Thr Tyr Ile Thr Glu Thr Glu Asp Val Phe
 355 360 365
 Tyr Thr Tyr Lys Gly Ser Leu Ala Pro Gln Asp Ser Asp Ser Glu Val
 370 375 380
 Ser Gln Asn Arg Ser Pro His Gln Glu Ser Leu Ser Glu Asn Asn Pro
 385 390 395 400
 Ala Gln Ser Tyr Leu Thr Gln Lys Ser Ser Ser Ser Val Ser Pro Ser
 405 410 415
 Ser Asn Ala Pro Gly Ser Cys Ser Pro Asp Gly Val Asp Gln Gln Leu
 420 425 430
 Leu Asp Asp Phe His Arg Val Thr Lys Gly Ser Thr Glu Asp Ala
 435 440 445
 Ser Gln Tyr Tyr Cys Asp Lys Asn Asp Asn Gly Asp Ser Tyr Leu Val
 450 455 460
 Leu Ile Arg Ile Thr Pro Asp Glu Asp Gly Lys Phe Gly Phe Asn Leu
 465 470 475 480
 Lys Gly Val Asp Gln Lys Met Pro Leu Val Val Ser Arg Ile Asn
 485 490 495
 Pro Glu Ser Pro Ala Asp Thr Cys Ile Pro Lys Leu Asn Glu Gly Asp
 500 505 510
 Gln Ile Val Leu Ile Asn Gly Arg Asp Ile Ser Glu His Thr His Asp
 515 520 525
 Gln Val Val Met Phe Ile Lys Ala Ser Arg Glu Ser His Ser Arg Glu
 530 535 540
 Leu Ala Leu Val Ile Arg Arg Arg Ala Val Arg Ser Phe Ala Asp Phe
 545 550 555 560
 Lys Ser Glu Asp Glu Leu Asn Gln Leu Phe Pro Glu Ala Ile Phe Pro
 565 570 575
 Met Cys Pro Glu Gly Gly Asp Thr Leu Glu Gly Ser Met Ala Gln Leu
 580 585 590

Lys Lys Gly Leu Glu Ser Gly Thr Val Leu Ile Gln Phe Glu Gln Leu
 595 600 605

Tyr Arg Lys Lys Pro Gly Leu Ala Ile Thr Phe Ala Lys Leu Pro Gln
 610 615 620

Asn Leu Asp Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr Asp Thr Thr
 625 630 635 640

Arg Val Leu Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val
 645 650 655

Asn Met Glu Ile Pro Ala Ala Asn Leu Val Asn Lys Tyr Ile Ala Thr
 660 665 670

Gln Gly Pro Leu Pro His Thr Cys Ala Gln Phe Trp Gln Val Val Trp
 675 680 685

Asp Gln Lys Leu Ser Leu Ile Val Met Leu Thr Thr Leu Thr Glu Arg
 690 695 700

Gly Arg Thr Lys Cys His Gln Tyr Trp Pro Asp Pro Pro Asp Val Met
 705 710 715 720

Asn His Gly Gly Phe His Ile Gln Cys Gln Ser Glu Asp Cys Thr Ile
 725 730 735

Ala Tyr Val Ser Arg Glu Met Leu Val Thr Asn Thr Gln Thr Gly Glu
 740 745 750

Glu His Thr Val Thr His Leu Gln Tyr Val Ala Trp Pro Asp His Gly
 755 760 765

Ile Pro Asp Asp Ser Ser Asp Phe Leu Glu Phe Val Asn Tyr Val Arg
 770 775 780

Ser Leu Arg Val Asp Ser Glu Pro Val Leu Val His Cys Ser Ala Gly
 785 790 795 800

Ile Gly Arg Thr Gly Val Leu Val Thr Met Glu Thr Ala Met Cys Leu
 805 810 815

Thr Glu Arg Asn Leu Pro Ile Tyr Pro Leu Asp Ile Val Arg Lys Met
 820 825 830

Arg Asp Gln Arg Ala Met Met Val Gln Thr Ser Ser Gln Tyr Lys Phe
 835 840 845

Val Cys Glu Ala Ile Leu Arg Val Tyr Glu Glu Gly Leu Val Gln Met
 850 855 860

Leu Asp Pro Ser
 865

<210> 27
 <211> 861
 <212> DNA
 <213> Homo sapiens

<220>
<223> human dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3) cDNA

<220>
<221> CDS
<222> (29)..(586)
<223> DUSP3

<400> 27
gccccggcgtg cagggccccc gccgcgcacat gtcgggctcg ttcgagctct cgggtgcagga 60
tctcaacgac ctgcctctcg acggcagcgg ctgctacagc ctcccgagcc agccctgcaa 120
cgaggtcacc ccgcgcgatct acgtgggcaa cggtctgtg gtcaggaca tccccaagct 180
gcagaaacta ggcatacaccat atgtgctgaa cgccgtctgag ggcaggctt tcattgcacgt 240
caacaccaat gccaacttct acaaggactc cggcatcaca tacctggca tcaaggccaa 300
cgacacacag gagttcaacc tcagcgctta ctttggaaagg gctgccact tcattgacca 360
ggctttggct caaaaagaatg gccgggtgct cgtccactgc cgggaagggtt atagccgctc 420
cccaaacgcta gttatcgctt acctcatgtat gccgcagaag atggacgtca agtctgccct 480
gagcatcggtt aggcagaacc gtgagatcg ccccaacgat ggcttcctgg cccagctctg 540
ccagctcaat gacagactag ccaaggaggg gaagttgaaa cccttagggca ccccccacccgc 600
ctctgctcgat gaggtccgtg ggggaggccc tggaaagggt gtccgagctg ccatgttttag 660
gaaacacact gtacctgtct cccagcatca caaggcactt gtctacaagt gtgtcccaac 720
acagtcctgg gccacttcc ccaccctggg gagcacataa agaagcttgc caagggggggc 780
gtccttgctc cccagttgtc ctgtttctgt aacttatgtat gtctttccc tgagatgggg 840
gctcagaggg ggaaggcctg t 861

<210> 28
<211> 185
<212> PRT
<213> Homo sapiens

<220>
<223> human dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3)

<400> 28
Met Ser Gly Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu
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Ser Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu
20 25 30

Val Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
35 40 45

Pro Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
50 55 60

Gly Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp
65 70 75 80

Ser Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe
85 90 95

Asn Leu Ser Ala Tyr Phe Glu Arg Ala Ala Asp Phe Ile Asp Gln Ala
100 105 110

Leu Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr
115 120 125

Ser	Arg	Ser	Pro	Thr	Leu	Val	Ile	Ala	Tyr	Leu	Met	Met	Arg	Gln	Lys
130															140
Met	Asp	Val	Lys	Ser	Ala	Leu	Ser	Ile	Val	Arg	Gln	Asn	Arg	Glu	Ile
145															160
Gly	Pro	Asn	Asp	Gly	Phe	Leu	Ala	Gln	Leu	Cys	Gln	Leu	Asn	Asp	Arg
					165				170						175
Leu	Ala	Lys	Glu	Gly	Lys	Leu	Lys	Pro							
					180				185						

<210> 29
<211> 1196
<212> DNA
<213> Mus musculus

<220>
<223> mouse dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3) cDNA

<220>
<221> CDS
<222> (64)..(621)
<223> DUSP3

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agcggctgtc acaggcctgcc gagccagccc tgcaacgagg tcgtcccgag ggtctacgtg 180
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cccacatctg tcccactctg gtcctcgcccc gcaactccac ccttagggag cacatgaaga 780
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<210> 30
<211> 185
<212> PRT
<213> Mus musculus

<220>
<223> mouse dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3)

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 20 25 30
 Val Val Pro Arg Val Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
 35 40 45
 Thr Gln Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
 50 55 60
 Gly Arg Ser Phe Met His Val Asn Thr Ser Ala Ser Phe Tyr Glu Asp
 65 70 75 80
 Ser Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe
 85 90 95
 Asn Leu Ser Ala Tyr Phe Glu Arg Ala Thr Asp Phe Ile Asp Gln Ala
 100 105 110
 Leu Ala His Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr
 115 120 125
 Ser Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys
 130 135 140
 Met Asp Val Lys Ser Ala Leu Ser Thr Val Arg Gln Asn Arg Glu Ile
 145 150 155 160
 Gly Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg
 165 170 175
 Leu Ala Lys Glu Gly Lys Val Lys Leu
 180 185

<210> 31
 <211> 753
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human regulator of G-protein signaling 10 (RGS10)
 cDNA

<220>
 <221> CDS
 <222> (133) .. (636)
 <223> RGS10

<400> 31
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 ggacaccaga gcatggaaaca catccacgac agcgatggca gttccagcag cagccaccag 180
 agcctaaga gcacagccaa atggcggca tccctggaga atctgctgga agacccagaa 240
 ggcgtgaaaa gatttaggaa atttttaaaa aaggaattca gtgaagaaaa tgttttgtt 300
 tggctagcat gtgaagattt taagaaaatg caagataaga cgccagatgca gaaaaaggca 360
 aaggagatct acatgacctt tctgtccagc aaggcctcat cacagtcaa cgtggagggg 420
 cagtctcgcc tcaacgagaa gatcctggaa gaacccgacc ctctgatgtt ccagaaactc 480

caggaccaga tcttaatct catgaagtac gacagctaca gccgcttct taagtctgac 540
ttgttttaa aacacaagcg aaccgaggaa gaggagaag atttgctga tgctcaaact 600
gcagctaaa gagctccag aatttataac acatgagccc ccaaaaagcc gggactggca 660
gctttagaa gcaaaggaa ttcctctcag gacgtgccgg gtttatcatt gctttgttat 720
ttgtaaggac tgaaatgtac aaaacccttc aat 753

<210> 32
<211> 167
<212> PRT
<213> Homo sapiens

<220>
<223> human regulator of G-protein signaling 10 (RGS10)

<400> 32
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Ser Leu Lys Ser Thr Ala Lys Trp Ala Ala Ser Leu Glu Asn Leu Leu
20 25 30

Glu Asp Pro Glu Gly Val Lys Arg Phe Arg Glu Phe Leu Lys Lys Glu
35 40 45

Phe Ser Glu Glu Asn Val Leu Phe Trp Leu Ala Cys Glu Asp Phe Lys
50 55 60

Lys Met Gln Asp Lys Thr Gln Met Gln Glu Lys Ala Lys Glu Ile Tyr
65 70 75 80

Met Thr Phe Leu Ser Ser Lys Ala Ser Ser Gln Val Asn Val Glu Gly
85 90 95

Gln Ser Arg Leu Asn Glu Lys Ile Leu Glu Glu Pro His Pro Leu Met
100 105 110

Phe Gln Lys Leu Gln Asp Gln Ile Phe Asn Leu Met Lys Tyr Asp Ser
115 120 125

Tyr Ser Arg Phe Leu Lys Ser Asp Leu Phe Leu Lys His Lys Arg Thr
130 135 140

Glu Glu Glu Glu Asp Leu Pro Asp Ala Gln Thr Ala Ala Lys Arg
145 150 155 160

Ala Ser Arg Ile Tyr Asn Thr
165

<210> 33
<211> 877
<212> DNA
<213> Mus musculus

<220>
<223> mouse regulator of G-protein signaling 10 (RGS10)
cDNA

<220>
 <221> CDS
 <222> (60)..(605)
 <223> RGS10

<400> 33
 gctcttcggg cttagccgcc gcgctgccc gctgctccgt cctctggacg cccgcggcga 60
 tgttcacccg cgccgtgagc cgactgagca ggaagcggcc gccgtctgat atccatgacg 120
 gagatgggag ctcaagcagc ggccaccaga gccttaagag cacagccaag tggcatcct 180
 ccctggagaa tcttctggaa gacccagaag gggtgagag attcaggag tttctgaaga 240
 aggaattcag cgaagagaat gtctgttt ggctagcgtg tgaagattc aagaaaacgg 300
 aggacaggaa gcagatgcag gaaaaggcca aggagatcta catgacccctc ctgtccaata 360
 aggcctcttc acaagtcaac gtggagggc agtctcggt cactgaaaag attctggaa 420
 agccacaccc tctgatgttc caaaagctcc aggaccagat cttcaatctc atgaagtatg 480
 acagctacag cgcgttcttg aagtctgact tgttctgaa acccaagcga actgaggaag 540
 aggaagaaga gccccccgat gctcagaccg cagctaagcg agcctccaga attacaaca 600
 cataagctga gcccttcacc ccagcgaagg agagggatgg actcttagga ctgtacaggc 660
 tgtcattttt ttgttgtgtt tgaggactgg agtgtgctag accttcctc tgatatgtg 720
 tattttatta actgaacagc aacctctgca tgatgctaattt cttccattaa aaacaaaagt 780
 agctttaaag tgtcagttca caaaaacaca tgagattctg ccaatactgg acactcagcc 840
 ttcatttc gattaaagtg ttcgtgaagc tacaagc 877

<210> 34
 <211> 181
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse regulator of G-protein signaling 10 (RGS10)

<400> 34
 Met Phe Thr Arg Ala Val Ser Arg Leu Ser Arg Lys Arg Pro Pro Ser
 1 5 10 15
 Asp Ile His Asp Gly Asp Gly Ser Ser Ser Ser Gly His Gln Ser Leu
 20 25 30
 Lys Ser Thr Ala Lys Trp Ala Ser Ser Leu Glu Asn Leu Leu Glu Asp
 35 40 45
 Pro Glu Gly Val Gln Arg Phe Arg Glu Phe Leu Lys Lys Glu Phe Ser
 50 55 60
 Glu Glu Asn Val Leu Phe Trp Leu Ala Cys Glu Asp Phe Lys Thr
 65 70 75 80
 Glu Asp Arg Lys Gln Met Gln Glu Lys Ala Lys Glu Ile Tyr Met Thr
 85 90 95
 Phe Leu Ser Asn Lys Ala Ser Ser Gln Val Asn Val Glu Gly Gln Ser
 100 105 110
 Arg Leu Thr Glu Lys Ile Leu Glu Glu Pro His Pro Leu Met Phe Gln
 115 120 125
 Lys Leu Gln Asp Gln Ile Phe Asn Leu Met Lys Tyr Asp Ser Tyr Ser
 130 135 140
 Arg Phe Leu Lys Ser Asp Leu Phe Leu Lys Pro Lys Arg Thr Glu Glu
 145 150 155 160

Glu Glu Glu Glu Pro Pro Asp Ala Gln Thr Ala Ala Lys Arg Ala Ser
 165 170 175
 Arg Ile Tyr Asn Thr
 180

<210> 35
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hexahistidine
 (His) affinity tag

<400> 35
 His His His His His His
 1 5

<210> 36
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:poly-Gly
 flexible linker

<220>
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly residues from position 6 to 200 may be present
 or absent

<400> 36
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 1 5 10 15
 Gly
 20 25 30
 Gly
 35 40 45
 Gly
 50 55 60
 Gly
 65 70 75 80
 Gly
 85 90 95
 Gly
 100 105 110
 Gly
 115 120 125

Gly
130 135 140

Gly
145 150 155 160

Gly
165 170 175

Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly
195 200